

AMENDMENTS TO THE CLAIMS

1-53. (Cancelled)

54. (Currently Amended) The transformant according to ~~claim 53~~ any one of claims 55 or 56, wherein the biosurfactant is ~~hydrophobin or a hydrophobin homologue derived from biosurfactant is encoded by the genome of Aspergillus oryzae~~.

55. (Currently Amended) ~~The transformant according to claim 54~~ A transformant comprising a nucleic acid sequence encoding a biosurfactant and a nucleic acid sequence encoding a plastic-degrading enzyme,

~~wherein the DNA comprising the gene nucleic acid sequence encoding the biosurfactant encodes a hydrophobin or a hydrophobin homologue is a DNA comprising a base sequence encoding the following polypeptide (a) or (b):~~

~~(a) polypeptide having an amino acid sequence that is the same or substantially the same as that represented by of SEQ ID NO:1, SEQ ID NO:2 or SEQ ID NO:3, or~~

~~(b) polypeptide having an amino acid sequence of (a) wherein a part of amino acid residues are replaced, deleted, or added, and having substantially the same function as the hydrophobin the amino acid sequence at least 90% identical to SEQ ID NO:1.~~

56. (Currently Amended) ~~The transformant according to claim 54~~ A transformant comprising a nucleic acid sequence encoding a biosurfactant and a nucleic acid sequence

encoding a plastic-degrading enzyme, wherein the DNA comprising the gene nucleic acid sequence encoding the biosurfactant comprises hydrophobin or hydrophobin homologue is a DNA of the following (a) or (b):

- (a) DNA comprising a base sequence represented by a nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2 or SEQ ID NO:3 or its partial sequence,;
- (b) DNA being hybridized a nucleotide sequence which hybridizes with a base nucleotide sequence complementary to the DNA comprising the base sequence in (a) full length of the nucleotide sequence of SEQ ID NO:1 under stringent conditions, and having substantially the same function as the DNA (a) comprising a sodium concentration of 900 mM and pH of 6 to a pH of 8 at 68°C; or
- (c) a nucleotide sequence at least 95% identical to SEQ ID NO:1.

57-59. (Cancelled)

60. (Currently Amended) The transformant according to claim 53 any one of claims 55 or 56, wherein the plastic-degrading enzyme is a serine hydrolase from encoded by the genome of *Aspergillus oryzae*.

61. (Previously Presented) The transformant according to claim 60, wherein the serine hydrolase is an esterase.

62. (Previously Presented) The transformant according to claim 61, wherein the esterase is a cutinase.

63-64. (Cancelled)

65. (Currently Amended) The transformant according to ~~claim 53~~ any one of claims 55 or 56, which [[is]] further ~~prepared by recombination with the use of~~ DNA comprising a gene comprises a nucleic acid sequence encoding a useful substance protein involved in a biosynthesis or an enzyme.

66. (Currently Amended) A transformant ~~prepared by recombination with the use of~~ the DNA comprising the gene a nucleic acid encoding [[the]] a hydrophobin derived from Aspergillus oryzae, the DNA comprising the gene, a nucleic acid encoding [[the]] a cutinase derived from Aspergillus oryzae, and a DNA comprising a gene nucleic acid encoding an amylase, wherein said hydrophobin and said cutinase are encoded by the genome of Aspergillus oryzae.

67. (Currently Amended) The transformant according to ~~claim 53~~ any one of claims 55 or 56, wherein at least one of the DNA comprising the gene nucleic acid encoding the biosurfactant and the DNA comprising the gene nucleic acid encoding the plastic-degrading enzyme is expressed under the control of a promoter ~~derived from another gene~~.

68. (Currently Amended) The transformant according to ~~claim 53~~ any one of claims 55 or 56, which is wherein the transformant organism is a eukaryotic filamentous fungus selected from the group consisting of ~~genera of~~: *Aspergillus*, *Penicillium*, *Trichoderma* *Trichoderma*, *Rhizopus*, *Magnaporthe*, *Metarhizium*, *Neurospora*, *Monascus*, *Acremonium* and *Mucor*.

69. (Currently Amended) The transformant according to claim 68, which is genera of wherein the transformant organism is *Aspergillus*.

70. (Currently Amended) The transformant according to claim 69, which is wherein the transformant organism is *Aspergillus oryzae*.

71. (New) The transformant according to any one of claims 55 or 66, wherein the hydrophobin comprises the amino acid sequence at least 99% identical to SEQ ID NO:1.

72. (New) The transformant according to any one of claims 55, 56 or 66, wherein the hydrophobin comprises a region having 100% sequence identity to SEQ ID NO:1.

73. (New) The transformant according to any one of claims 55 or 56, wherein the plastic degrading enzyme is selected from the group consisting of: esterase, protease, peptidase, lipase, cutinase and serine hydrolase.